



## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: SCHENDEL, Dolores J.
- (ii) TITLE OF INVENTION: T CELLS SPECIFIC FOR KIDNEY CARCINOMA
- (iii) NUMBER OF SEQUENCES: 45
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Nikaido, Marmelstein, Murray and Oram LLP
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  - (C) CITY: Washington
  - (D) STATE: DC
  - (E) COUNTRY: USA
  - (F) ZIP: 20005-5701
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/881,509
  - (B) FILING DATE: June 24, 1997
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Kitts, Monica Chin
  - (B) REGISTRATION NUMBER: 36,105
  - (C) REFERENCE/DOCKET NUMBER: 564-7015
- (ix) TELECOMMUNICATION INFORMATION:
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## (2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1341 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..801
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: 1..54
- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide

(B) LOCATION:55..801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG AGG CAA GTG GCG AGA GTG ATC GTG TTC CTG ACC CTG AGT ACT TTG Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu -18                      -15                      -10                      -5	48
AGC CTT GCT AAG ACC ACC CAG CCC ATC TCC ATG GAC TCA TAT GAA GGA Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly 1                      5                      10	96
CAA GAA GTG AAC ATA ACC TGT AGC CAC AAC AAC ATT GCT ACA AAT GAT Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp 15                      20                      25                      30	144
TAT ATC ACG TGG TAC CAA CAG TTT CCC AGC CAA GGA CCA CGA TTT ATT Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile 35                      40                      45	192
ATT CAA GGA TAC AAG ACA AAA GTT ACA AAC GAA GTG GCC TCC CTG TTT Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe 50                      55                      60	240
ATC CCT GCC GAC AGA AAG TCC AGC ACT CTG AGC CTG CCC CGG GTT TCC Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser 65                      70                      75	288
CTG AGC GAC ACT GCT GTG TAC TAC TGC CTC GTG GGT GGT TCT GCA AGG Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg 80                      85                      90	336
CAA CTG ACC TTT GGA TCT GGG ACA CAA TTG ACT GTT TTA CCT GAT ATC Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile 95                      100                      105                      110	384
CAG AAC CCT GAC CCT GCC GTG TAC CAG CTG AGA GAC TCT AAA TCC AGT Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser 115                      120                      125	432
GAC AAG TCT GTC TGC CTA TTC ACC GAT TTT GAT TCT CAA ACA AAT GTG Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val 130                      135                      140	480
TCA CAA AGT AAG GAT TCT GAT GTG TAT ATC ACA GAC AAA ACT GTG CTA Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu 145                      150                      155	528
GAC ATG AGG TCT ATG GAC TTC AAG AGC AAC AGT GCT GTG GCC TGG AGC Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser 160                      165                      170	576
AAC AAA TCT GAC TTT GCA TGT GCA AAC GCC TTC AAC AAC AGC ATT ATT Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile 175                      180                      185                      190	624
CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys 195                      200                      205	672

CTG GTC GAG AAA AGC TTT GAA ACA GAT ACG AAC CTA AAC TTT CAA AAC Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn 210 215 220	720
CTG TCA GTG ATT GGG TTC CGA ATC CTC CTC CTG AAA GTG GCC GGG TTT Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe 225 230 235	768
AAT CTG CTC ATG ACG CTG CGG CTG TGG TCC AGC TGAGATCTGC AAGATTGTAA Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser 240 245	821
GACAGCCTGT GCTCCCTCGC TCCTTCCTCT GCATTGCCCC TCTTCTCCCT CTCCAAACAG	881
AGGGAACTCT CCTACCCCCA AGGAGGTGAA AGCTGCTACC ACCTCTGTGC CCCCCGGCA	941
ATGCCACCAA CTGGATCCTA CCCGAATTTA TGATTAAGAT TGCTGAAGAG CTGCCAAACA	1001
CTGCTGCCAC CCCCTCTGTT CCCTTATTGC TGCTTGTCAC TGCCTGACAT TCACGGCAGA	1061
GGCAAGGCTG CTGCAGCCTC CCCTGGCTGT GCACATTCCC TCCTGCTCCC CAGAGACTGC	1121
CTCCGCCATC CCACAGATGA TGGATCTTCA GTGGGTTCTC TTGGGCTCTA GGTCTGGAG	1181
AATGTTGTGA GGGGTTTATT TTTTTTTAAT AGTGTTTATA AAGAAATACA TAGTATTCTT	1241
CTTCTCAAGA CGTGGGGGGA AATTATCTCA TTATCGAGGC CCTGCTATGC TGTGTGTCTG	1301
GGCGTGTGTG ATGTCCTGCT GCCGATGCCT TCATTAAAT	1341

## (2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu -18 -15 -10 -5
Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly 1 5 10
Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp 15 20 25 30
Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile 35 40 45
Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe 50 55 60
Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser 65 70 75

Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg  
 80 85 90  
 Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile  
 95 100 105 110  
 Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser  
 115 120 125  
 Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val  
 130 135 140  
 Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu  
 145 150 155  
 Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser  
 160 165 170  
 Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile  
 175 180 185 190  
 Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys  
 195 200 205  
 Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn  
 210 215 220  
 Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe  
 225 230 235  
 Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser  
 240 245

## (2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 936 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..933

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION:1..63

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION:64..933

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG GAT ACC TGG CTC GTA TGC TGG GCA ATT TTT AGT CTC TTG AAA GCA  
 Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala  
 -21 -20 -15 -10

GGA CTC ACA GAA CCT GAA GTC ACC CAG ACT CCC AGC CAT CAG GTC ACA Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr -5 1 5 10	96
CAG ATG GGA CAG GAA GTG ATC TTG CGC TGT GTC CCC ATC TCT AAT CAC Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His 15 20 25	144
TTA TAC TTC TAT TGG TAC AGA CAA ATC TTG GGG CAG AAA GTC GAG TTT Leu Tyr Phe Tyr Trp Tyr Arg Gln Ile Leu Gly Gln Lys Val Glu Phe 30 35 40	192
CTG GTT TCC TTT TAT AAT AAT GAA ATC TCA GAG AAG TCT GAA ATA TTC Leu Val Ser Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe 45 50 55	240
GAT GAT CAA TTC TCA GTT GAA AGG CCT GAT GGA TCA AAT TTC ACT CTG Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu 60 65 70 75	288
AAG ATC CGG TCC ACA AAG CTG GAG GAC TCA GCC ATG TAC TTC TGT GCC Lys Ile Arg Ser Thr Lys Leu Glu Asp Ser Ala Met Tyr Phe Cys Ala 80 85 90	336
AGC AGC GAA ACT AAC TCC TAC GAG CAG TAC TTC GGG CCG GGC ACC AGG Ser Ser Glu Thr Asn Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg 95 100 105	384
CTC ACG GTC ACA GAG GAC CTG AAA AAC GTG TTC CCA CCC GAG GTC GCT Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala 110 115 120	432
GTG TTT GAG CCA TCA GAA GCA GAG ATC TCC CAC ACC CAA AAG GCC ACA Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr 125 130 135	480
CTG GTG TGC CTG GCC ACA GGC TTC TAC CCC GAC CAC GTG GAG CTG AGC Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser 140 145 150 155	528
TGG TGG GTG AAT GGG AAG GAG GTG CAC AGT GGG GTC AGC ACA GAC CCG Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro 160 165 170	576
CAG CCC CTC AAG GAG CAG CCC GCC CTC AAT GAC TCC AGA TAC TGC CTG Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu 175 180 185	624
AGC AGC CGC CTG AGG GTC TCG GCC ACC TTC TGG CAG AAC CCC CGC AAC Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn 190 195 200	672
CAC TTC CGC TGT CAA GTC CAG TTC TAC GGG CTC TCG GAG AAT GAC GAG His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu 205 210 215	720
TGG ACC CAG GAT AGG GCC AAA CCT GTC ACC CAG ATC GTC AGC GCC GAG Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu 220 225 230 235	768

GCC TGG GGT AGA GCA GAC TGT GGC TTC ACC TCC GAG TCT TAC CAG CAA	816
Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln	
240 245 250	
GGG GTC CTG TCT GCC ACC ATC CTC TAT GAG ATC TTG CTA GGG AAG GCC	864
Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala	
255 260 265	
ACC TTG TAT GCC GTG CTG GTC AGT GCC CTC GTG CTG ATG GCC ATG GTC	912
Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val	
270 275 280	
AAG AGA AAG GAT TCC AGA GGC TAG	936
Lys Arg Lys Asp Ser Arg Gly	
285 290	

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala	
-21 -20 -15 -10	
Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr	
-5 1 5 10	
Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His	
15 20 25	
Leu Tyr Phe Tyr Trp Tyr Arg Gln Ile Leu Gly Gln Lys Val Glu Phe	
30 35 40	
Leu Val Ser Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe	
45 50 55	
Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu	
60 65 70 75	
Lys Ile Arg Ser Thr Lys Leu Glu Asp Ser Ala Met Tyr Phe Cys Ala	
80 85 90	
Ser Ser Glu Thr Asn Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg	
95 100 105	
Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala	
110 115 120	
Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr	
125 130 135	
Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser.	

140		145		150		155									
Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro
			160						165					170	
Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu
		175						180					185		
Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn
		190					195					200			
His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu
	205					210					215				
Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu
220					225					230					235
Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr	Gln	Gln
			240						245					250	
Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala
		255						260					265		
Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val
	270						275					280			
Lys	Arg	Lys	Asp	Ser	Arg	Gly									
285						290									

## (2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..39

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGC	CTC	GTC	CTT	TCT	GGT	TCT	GCA	AGG	CAA	CTG	ACC	TTT
Cys	Leu	Val	Leu	Ser	Gly	Ser	Ala	Arg	Gln	Leu	Thr	Phe
			295						300			

39

## (2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein.

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(A) NAME/KEY: CDS  
(B) LOCATION: 1..36

TGC	CTC	GCT	ACT	GGT	TCT	GCA	AGG	CAA	CTG	ACC	TTT
Cys	Leu	Ala	Thr	Gly	Ser	Ala	Arg	Gln	Leu	Thr	Phe
	15					20					25

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

Cys Leu Ala Thr Gly Ser Ala Arg Gln Leu Thr Phe  
1 5 10

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: linear

(A) NAME/KEY: CDS  
(B) LOCATION: 1..39

TGT GCC AGC AGT GGA ACA GAT TCC TAC GAG CAG TAC TTC  
Cys Ala Ser Ser Gly Thr Asp Ser Tyr Glu Gln Tyr Phe  
15 20 25

(2) INFORMATION FOR SEQ ID NO: 10:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Cys Ala Ser Ser Gly Thr Asp Ser Tyr Glu Gln Tyr Phe  
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION:1..39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TGT GCC AGC AGT GAA ACA GAT TCC TAC GAG CAG TAC TTC  
 Cys Ala Ser Ser Glu Thr Asp Ser Tyr Glu Gln Tyr Phe  
 15 20 25

39

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Cys Ala Ser Ser Glu Thr Asp Ser Tyr Glu Gln Tyr Phe  
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION:1..39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TGT GCC AGC AGT GGA ACA GCT TCC TAC GAG CAG TAC TTC  
Cys Ala Ser Ser Gly Thr Ala Ser Tyr Glu Gln Tyr Phe  
15 20 25

39

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Cys Ala Ser Ser Gly Thr Ala Ser Tyr Glu Gln Tyr Phe  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION:1..39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TGT GCC AGC AGT GGT ACA AAC TCC TAC GAG CAG TAC TTT  
Cys Ala Ser Ser Gly Thr Asn Ser Tyr Glu Gln Tyr Phe  
15 20 25

39

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Cys Ala Ser Ser Gly Thr Asn Ser Tyr Glu Gln Tyr Phe  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..39

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TGT GCC ACC TCC GGG ACA GCT TCC TAC GAG CAG TAC TTC  
 Cys Ala Thr Ser Gly Thr Ala Ser Tyr Glu Gln Tyr Phe  
       15                              20                              25

39

## (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Cys Ala Thr Ser Gly Thr Ala Ser Tyr Glu Gln Tyr Phe  
       1                              5                              10

## (2) INFORMATION FOR SEQ ID NO: 19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..39

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGT GCC AGA TCC GGG ACA GGC TCC TAC GAG CAG TAC TTC  
 Cys Ala Arg Ser Gly Thr Gly Ser Tyr Glu Gln Tyr Phe  
       15                              20                              25

39

## (2) INFORMATION FOR SEQ ID NO: 20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Cys Ala Arg Ser Gly Thr Gly Ser Tyr Glu Gln Tyr Phe  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CACTGAAGAT CCATCATCTG

20

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22;

TAGAGGATGG TGGCAGACAG

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 4..8

(C) OTHER INFORMATION: /note= "Xaa(1) to Xaa(5) represents a sequence of 3 to 5 amino acids

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Tyr Cys Leu Xaa Xaa Xaa Xaa Ser Ala Arg Gln Leu Thr Phe  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 14 amino acids  
 (B) TYPE: amino acid

- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 3..9
- (C) OTHER INFORMATION: /note= "Xaa(1) to Xaa(7) represents a sequence of 5 to 7 amino acids"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Cys Ala Xaa Xaa Xaa Xaa Xaa Xaa Tyr Glu Gln Tyr Phe  
1 5 10

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 3..9
- (C) OTHER INFORMATION: /note= "Xaa(1) to Xaa(7) represents a sequence of 5 to 7 amino acids"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Cys Ala Xaa Xaa Xaa Xaa Xaa Xaa Asn Glu Gln Phe Phe  
1 5 10

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 3..9
- (C) OTHER INFORMATION: /note= "Xaa(1) to Xaa(7) represents a sequence of 5 to 7 amino acids"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys Ala Xaa Xaa Xaa Xaa Xaa Xaa Asp Thr Gln Tyr Phe  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ser Ser Glu Thr Asn Ser  
1 5

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ser Ser Glu Thr Ser Ser  
1 5

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Thr Ser Gly Thr Ala Ser  
1 5

## (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Arg Ser Gly Thr Gly Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ser Ser Gly Thr Asp Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ser Ser Gly Thr Arg Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ser Ser Gly Ser Asp Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser Ser Ser Thr Gly Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ser Ser Ser Thr Val Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser Ser Ser Thr Leu Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ser Ser Ser Thr Leu Phe  
1 5



## (2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ser Ser Ser Thr Ala Ser  
1 5

## (2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Ser His Thr Asp Ser  
1 5

## (2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Ser Ser Asp Thr Leu Ser  
1 5

## (2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ser Arg Trp Asp Ser Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Ser Ser Gly Thr Ser Ser Tyr  
1 5

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser Ser Asp Gln Gly Met  
1 5

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ser Ala Asp Ser Phe Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant